

IN THE CLAIMS

Please amend claims 1, 3, 7, 10, 12, 13, 19-21, and 43, and insert new claims 44-56, as follows:

1. (Currently Amended) A method for ~~classifyinganalyzing~~ chromatograms, comprising:
receiving a first chromatogram data;
adjusting the first chromatogram data in a first region of interest;
reducing the first chromatogram data to a first data set, ~~wherein the first chromatogram data is reduced based upon a consistent positioning across chromatograms based at least on an average time for the chromatogram data in the first region of interest~~;
receiving a second chromatogram data;
adjusting the second chromatogram data in a second region of interest;
reducing the second chromatogram data to a second data set, ~~wherein the second chromatogram data is reduced based upon the consistent positioning across chromatograms based at least on an average time for the chromatogram data in the second region of interest~~; and
comparing the first data set and the second data set.

2. (Original) The method of claim 1 in which the acts of adjusting the first and second chromatogram data comprise baseline correction.

3. (Currently Amended) The method of claim 1 further comprising:
~~identifying a first chromatogram~~ the first region of interest in the first chromatogram data;
and
~~identifying a second chromatogram~~ the second region of interest in the second chromatogram

data.

4. (Original) The method of claim 1 in which the act of adjusting data in the first and second regions of interest comprises centering an analysis window around one or more trace features in a given region of interest.

5. (Original) The method of claim 4 in which the act of centering comprises:
determining an average time for the given region of interest; and
centering the analysis window around the average time.

6. (Original) The method of claim 1 further comprising:
filtering the first and second chromatogram data to identify bad data.

7. (Currently Amended) The method of claim 6 in which the ~~act of~~ filtering is based upon criteria selected from a group consisting of: peak height, peak area, peak shape, peak position, peak slope, and peak size.

8. (Original) The method of claim 1 in which the acts of reducing the first and second chromatogram data to the first and second data sets comprise determining arrays of data set values directly from the first and second chromatogram data.

9. (Original) The method of claim 1 in which the acts of reducing the first and second chromatogram data to the first and second data sets comprise:

determining an integral of the first and second chromatogram data and plotting against a time axis;

determining a set of time points; and

forming arrays of data set values based upon the set of time points and corresponding integral values for the set of time points.

10. (Currently Amended) The method of claim 1 further comprising:

selecting a reference chromatogram to be compared with one or both of the first and second chromatogram data.

11. (Original) The method of claim 10 in which the reference chromatogram is selected based upon first selecting a plurality of chromatograms having one or more identified characteristics that most closely match one or more reference characteristics, and identifying a single chromatogram within the plurality of chromatograms to be the reference chromatogram.

12. (Currently Amended) The method of claim 10 in which other chromatograms one or both of the first and second chromatogram data are compared against the reference chromatogram.

13. (Currently Amended) The method of claim 12 further comprising:

mapping results of comparing the reference chromatogram against the other chromatograms one or both of the first and second chromatogram data.

14. (Original) The method of claim 13 in which mapping is performed to a two-dimensional

cluster map.

15. (Original) The method of claim 1 in which the act of comparing comprises determining a degree of similarity between the first and second data sets.

16. (Original) The method of claim 1 in which the act of comparing comprises determining a degree of dissimilarity between the first and second data sets.

17. (Original) The method of claim 1 in which the act of comparing comprises determining distance between vectors associated with the first and second data sets.

18. (Original) The method of claim 1 in which the first and second chromatogram data relate to DNA analysis, wherein the reduced chromatogram data excludes a main DNA peak and fully encapsulate a possible sequence variation peak.

19. (Currently Amended) A system for ~~classifying~~^{analyzing} chromatograms, comprising:
a data storage device to store chromatogram data;
a communications interface adaptable to receive chromatogram data from the data storage device;
a data adjustment module to adjust the chromatogram data;
a reduction module to reduce the chromatogram data to a data set ~~that can be compared~~
~~against other chromatogram data sets based at least on an average time for the chromatogram data in~~
~~a region of interest;~~ and

a comparison module to compare the data set against the other chromatogram data sets.

20. (Currently Amended) The system of claim 19 further comprising a ~~bad~~-data filter.

21. (Currently Amended) The system of claim 20 in which the ~~bad~~-data filter performs filtering based upon criteria selected from the group consisting of: peak height, peak area, peak shape, peak position, peak slope, and peak size.

22. (Original) The system of claim 19 in which the data adjustment module performs baseline correction for the chromatogram data in a region of interest.

23. (Original) The system of claim 19 in which the data adjustment module centers the analysis window around one or more trace features in a region of interest.

24. (Original) The system of claim 19 in which the reduction module determines an array of data set values directly from the chromatogram data.

25. (Original) The system of claim 24 in which the array of data set values are formed by:
selecting a set of time points in the first and second chromatogram data;
determining amplitude values corresponding to the set of time points; and
forming the arrays of data set values based upon the set of time points and their corresponding amplitude values.

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26. (Original) The system of claim 19 in which the reduction module determines an array of data set values based upon:

determining an integral of the chromatogram data and plotting against a time axis;

determining a set of time points;

forming the arrays of data set values based upon the set of time points and corresponding integral values for the set of time points.

27. (Original) The system of claim 19 implemented using one or more programmable logic devices.

28. (Original) The system of claim 19 further comprising a mapping module to map results from the comparison module.

29. (Original) The system of claim 28 further comprising a user interface to display results from the comparison module.

30-42. (Withdrawn)

43. (Currently Amended) A computer usable medium having stored thereon a sequence of instructions which, when executed by a processor, causes the processor to execute a process ~~for classifying chromatograms~~, said process comprising:

receiving a first chromatogram data;

adjusting the first chromatogram data in a first region of interest;

reducing the first chromatogram data to a first data set, ~~wherein the first chromatogram data is reduced based a consistent positioning across chromatograms based at least on an average time for the chromatogram data in the first region of interest;~~

receiving a second chromatogram data;

adjusting the second chromatogram data in a second region of interest;

reducing the second chromatogram data to a second data set, ~~wherein the second chromatogram data is reduced based upon the consistent positioning across chromatograms based at least on an average time for the chromatogram data in the second region of interest;~~ and

comparing the first data set and the second data set.

44. (New) The method of claim 1, further comprising determining the average time for chromatogram data in the first region of interest, and determining the average time for chromatogram data in the second region of interest.

45. (New) The method of claim 44, wherein the determining the average time for chromatogram data in the first and second regions of interest is performed based on $\bar{t} = (\sum_{i=0}^{i=n} y_i^2 * t_i) / \sum_{i=0}^{i=n} y_i^2$.

46. (New) A computer usable medium having stored thereon a set of instructions which, when executed by a processor, causes the processor to execute a process, the process comprising:

receiving a first chromatogram data;

identifying a first region of interest in the first chromatogram data;

positioning the first region of interest based at least on an average time for the chromatogram

data in the first region of interest;

reducing chromatogram data in the first region to a first data set;

receiving a second chromatogram data;

identifying a second region of interest in the second chromatogram data;

positioning the second region of interest based at least on an average time for the chromatogram data in the second region of interest;

reducing chromatogram data in the second region of interest to a second data set; and

comparing the first data set and the second data set.

47. (New) The computer usable medium of claim 46, wherein the process further comprising determining the average time for chromatogram data in the first region of interest, and determining the average time for chromatogram data in the second region of interest.

48. (New) The computer usable medium of claim 47, wherein the determining the average time for chromatogram data in the first and second regions of interest is performed based on

$$\bar{t} = \left(\sum_{i=0}^{i=n} y_i^2 * t_i \right) / \sum_{i=0}^{i=n} y_i^2 .$$

49. (New) A method for analyzing chromatograms, comprising:

receiving a first chromatogram data;

identifying a first region of interest in the first chromatogram data;

positioning the first region of interest without explicitly identifying a peak within the first region of interest;

reducing chromatogram data in the first region to a first data set;
receiving a second chromatogram data;
identifying a second region of interest in the second chromatogram data;
positioning the second region of interest without explicitly identifying a peak within the second region of interest;
reducing chromatogram data in the second region of interest to a second data set; and
comparing the first data set and the second data set.

50. (New) The method of claim 49, wherein the positioning the first region of interest comprises determining an average time for chromatogram data in the first region of interest, and the positioning the second region of interest comprises determining an average time for chromatogram data in the second region of interest.

51. (New) The method of claim 50, wherein the determining the average time for chromatogram data in the first and second regions of interest is performed based on $\bar{t} = (\sum_{i=0}^{i=n} y_i^2 * t_i) / \sum_{i=0}^{i=n} y_i^2$.

52. (New) The method of claim 49, further comprising determining a first average positional line associated with the first chromatogram data, and determining a second average positional line associated with the second chromatogram data.

53. (New) The method of claim 52, wherein the positioning the first region of interest comprises shifting the first region of interest such that the first average positional line is located at a center of

the first region of interest, and the positioning the second region of interest comprises shifting the second region of interest such that the second average positional line is located at a center of the second region of interest.

54. (New) A computer usable medium having stored thereon a set of instructions which, when executed by a processor, causes the processor to execute a process, the process comprising:

- receiving a first chromatogram data;
- identifying a first region of interest in the first chromatogram data;
- positioning the first region of interest without explicitly identifying a peak within the first region of interest;
- reducing chromatogram data in the first region to a first data set;
- receiving a second chromatogram data;
- identifying a second region of interest in the second chromatogram data;
- positioning the second region of interest without explicitly identifying a peak within the second region of interest;
- reducing chromatogram data in the second region of interest to a second data set; and
- comparing the first data set and the second data set.

55. (New) The computer usable medium of claim 54, wherein the process further comprising determining the average time for chromatogram data in the first region of interest, and determining the average time for chromatogram data in the second region of interest.

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56. (New) The computer usable medium of claim 55, wherein the determining the average time

for chromatogram data in the first and second regions of interest is performed based on

$$\bar{t} = \left(\sum_{i=0}^{i=n} y_i^2 * t_i \right) / \sum_{i=0}^{i=n} y_i^2 .$$